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RAW SEQUENCE LISTING

DATE: 03/29/2002

PATENT APPLICATION: US/09/761,534A

TIME: 13:40:16

Input Set : A:\0399.2006-003SUBSEQLIST.TXT

Output Set: N:\CRF3\03292002\I761534A.raw

4 <110> APPLICANT: Huang, Qian
5 Richmond, Joan F.L.
6 Cho, Bryan K.
7 Palliser, Deborah
8 Chen, Jianzhu
9 Eisen, Herman N.
10 Young, Richard A.
12 <120> TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
13 Protein Fusion Proteins Maps To A Discrete Domain and is
14 CD4+T Cell-Independent
17 <130> FILE REFERENCE: 0399.2006-003
19 <140> CURRENT APPLICATION NUMBER: US 09/761,534A
20 <141> CURRENT FILING DATE: 2001-01-16
22 <150> PRIOR APPLICATION NUMBER: PCT/US00/32831
23 <151> PRIOR FILING DATE: 2000-12-01
25 <150> PRIOR APPLICATION NUMBER: US 60/176,143
26 <151> PRIOR FILING DATE: 2000-01-14
28 <160> NUMBER OF SEQ ID NOS: 25
30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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33 <211> LENGTH: 8
34 <212> TYPE: PRT
35 <213> ORGANISM: Unknown
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Peptide Liberated From P1
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42 1 5
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58 <210> SEQ ID NO: 3
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60 <212> TYPE: PRT
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63 <220> FEATURE:
64 <223> OTHER INFORMATION: Alpha KG Peptide

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68 1 5
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81 1 5
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87 <213> ORGANISM: Unknown
89 <220> FEATURE:
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92 <220> FEATURE:
93 <221> NAME/KEY: CDS
94 <222> LOCATION: (1)...(1260)
98 <400> SEQUENCE: 5
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100 Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
101 1 5 10 15
103 tcg gtt ctg gaa ggt ggc gac ccg gtc gtc gtc gcc aac tcc gag ggc 96
104 Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
105 20 25 30
107 tcc agg acc acc ccg tca att gtc gcg ttc gcc cgc aac ggt gag gtg 144
108 Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
109 35 40 45
111 ctg gtc ggc cag ccc gcc aag aac cag gca gtg acc aac gtc gat cgc 192
112 Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
113 50 55 60
115 acc gtg cgc tcg gtc aag cga cac atg ggc agc gac tgg tcc ata gag 240
116 Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu
117 65 70 75 80
119 att gac ggc aag aaa tac acc gcg ccg gag atc agc gcc cgc att ctg 288
120 Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu
121 85 90 95
123 atg aag ctg aag cgc gac gcc gag gcc tac ctc ggt gag gac att acc 336
124 Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr
125 100 105 110
127 gac gcg gtt atc acg acg ccc gcc tac ttc aat gac gcc cag cgt cag 384
128 Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln
129 115 120 125
131 gcc acc aag gac gcc ggc cag atc gcc ggc ctc aac gtg ctg cgg atc 432
132 Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
133 130 135 140

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135 gtc aac gag ccg acc gcg gcc gcg ctg gcc tac ggc ctc gac aag ggc 480
136 Val Asn Glu Pro Thr Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly
137 145 150 155 160
139 gag aag gag cag cga atc ctg gtc ttc gac ttg ggt ggt ggc act ttc 528
140 Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
141 165 170 175
143 gac gtt tcc ctg ctg gag atc ggc gag ggt gtg gtt gag gtc cgt gcc 576
144 Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
145 180 185 190
147 act tcg ggt gac aac cac ctc ggc ggc gac gac tgg gac cag cgg gtc 624
148 Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
149 195 200 205
151 gtc gat tgg ctg gtg gac aag ttc aag ggc acc agc ggc atg gat ctg 672
152 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
153 210 215 220
155 acc aag gac aag atg gcg atg cag cgg ctg cgg gaa gcc gcc gag aag 720
156 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
157 225 230 235 240
159 gca aag atc gag ctg agt tcg agt cag tcc acc tcg atc aac ctg ccc 768
160 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
161 245 250 255
163 tac atc acc gtc gac gcc gac aag aac ccg ttg ttc tta gac gag cag 816
164 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
165 260 265 270
167 ctg acc cgc gcg gag ttc caa cgg atc act cag gac ctg ctg gac cgc 864
168 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
169 275 280 285
171 act cgc aag ccg ttc cag tcg gtg atc gct gac acc ggc att tcg gtg 912
172 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val
173 290 295 300
175 tcg gag atc gat cac gtt gtg ctc gtg ggt ggt tcg acc cgg atg ccc 960
176 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
177 305 310 315 320
179 gcg gtg acc gat ctg gtc aag gaa ctc acc ggc ggc aag gaa ccc aac 1008
180 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
181 325 330 335
183 aag ggc gtc aac ccc gat gag gtt gtc gcg gtg gga gcc gct ctg cag 1056
184 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
185 340 345 350
187 gcc ggc gtc ctc aag ggc gag gtg aaa gac gtt ctg ctg ctt gat gtt 1104
188 Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
189 355 360 365
191 acc ccg ctg agc ctg ggt atc gag acc aag ggc ggg gtg atg acc agg 1152
192 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Arg
193 370 375 380
195 ctc atc gag cgc aac acc acg atc ccc acc aag cgg tcg gag act ttc 1200
196 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
197 385 390 395 400
199 acc acc gcc gac gac aac caa ccg tcg gtg cag atc cag gtc tat cag 1248

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200 Thr Thr Ala Asp Asp Asn Gln Pro Ser Val Gln Ile Gln Val Tyr Gln
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203 ggg gag cgt gag
204 Gly Glu Arg Glu
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209 <211> LENGTH: 420
210 <212> TYPE: PRT
211 <213> ORGANISM: Unknown
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Mycobacterium Tuberculosis hsp70 cDNA
217 <400> SEQUENCE: 6
218 Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
219 1 5 10 15
220 Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
221 20 25 30
222 Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
223 35 40 45
224 Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
225 50 55 60
226 Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu
227 65 70 75 80
228 Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu
229 85 90 95
230 Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr
231 100 105 110
232 Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln
233 115 120 125
234 Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
235 130 135 140
236 Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly
237 145 150 155 160
238 Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
239 165 170 175
240 Asp Val Ser Leu Leu Glu Ile Gly Glu Val Val Glu Val Arg Ala
241 180 185 190
242 Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
243 195 200 205
244 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
245 210 215 220
246 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
247 225 230 235 240
248 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
249 245 250 255
250 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
251 260 265 270
252 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
253 275 280 285
254 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val

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255      290      295      300
256 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
257 305      310      315      320
258 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
259      325      330      335
260 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
261      340      345      350
262 Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
263      355      360      365
264 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Arg
265      370      375      380
266 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
267 385      390      395      400
268 Thr Thr Ala Asp Asp Asn Gln Pro Ser Val Gln Ile Gln Val Tyr Gln
269      405      410      415
270 Gly Glu Arg Glu
271      420
274 <210> SEQ ID NO: 7
275 <211> LENGTH: 630
276 <212> TYPE: DNA
277 <213> ORGANISM: Unknown
279 <220> FEATURE:
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282 <221> NAME/KEY: CDS
283 <222> LOCATION: (1)...(630)
284 <223> OTHER INFORMATION: Segment II of TBhsp70
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290 1 5 10 15
292 gac gtt tcc ctg ctg gag atc ggc gag ggt gtg gtt gag gtc cgt gcc 96
293 Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
294 20 25 30
296 act tcg ggt gac aac cac ctc ggc ggc gac gac tgg gac cag cgg gtc 144
297 Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val
298 35 40 45
300 gtc gat tgg ctg gtg gac aag ttc aag ggc acc agc ggc atg gat ctg 192
301 Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
302 50 55 60
304 acc aag gac aag atg gcg atg cag cgg ctg cgg gaa gcc gcc gag aag 240
305 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
306 65 70 75 80
308 gca aag atc gag ctg agt tcg agt cag tcc acc tcg atc aac ctg ccc 288
309 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
310 85 90 95
312 tac atc acc gtc gac gcc gac aag aac ccg ttg ttc tta gac gag cag 336
313 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
314 100 105 110
316 ctg acc cgc gcg gag ttc caa cgg atc act cag gac ctg ctg gac cgc 384

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VERIFICATION SUMMARY

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